

Input file Fbh21620fl.seq; Output File 21620.trans  
Sequence length 1909

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TACTTAGACTCAGCCGGCTTTTCCACGCTTTGCCTGACCTGCTTTGCTCAACTGTACGCTTGTTCGTTTTCTGTTTC
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CCGGATCCGGTGATCCAAATCTAAGAACTGCTCCTCAGTGAGTGTTCGCTTTACTTCTAGGCCTGTACGGAAGTGTAC
TTCTGCTCTAAAAGCTGCGGAATTCTAATACGACTCACTATAGGGAGTCGACCCACGGCTCCGGGGTCTAGGCGCGGAT
CGGACCCAAGCAGGTTCGGCGCGCGGCGGAGAGAGCGGCGGCGGTCAGCTCCTCGACCCCCGTGTCGGGGCTAGTCCAG
      M A R P G M E R W R D R L
CGAGGCGGACGGGCGGCGTGGGCCC ATG GCC AGG CCC GGC ATG GAG CGG TGG CGC GAC CGG CTG 13
      39
A L V T G A S G G I G A A V A R A L V Q 33
CGC CTG GTG ACG GGG GCC TCG GGG GGC ATC GGC GCG GCC GTG GCC CGG GCC CTG GTC CAG 99
Q G L K V V G C A R T V G N I E E L A A 53
CAG GGA CTG AAG GTG GTG GGC TGC GCC CGC ACT GTG GGC AAC ATC GAG GAG CTG GCT GCT 159
E C K S A G Y P G T L I P Y R C D L S N 73
GAA TGT AAG AGT GCA GGC TAC CCC GGG ACT TTG ATC CCC TAC AGA TGT GAC CTA TCA AAT 219
E E D I L S M F S A I R S Q H S G V D I 93
GAA GAG GAC ATC CTC TCC ATG TTC TCA GCT ATC CGT TCT CAG CAC AGC GGT GTA GAC ATC 279
C I N N A G L A R P D T L L S G S T S G 113
TGC ATC AAC AAT GCT GGC TTG GCC CGG CCT GAC ACC CTG CTC TCA GGC AGC ACC AGT GGT 339
W K D M F N V N V L A L S I C T R E A Y 133
TGG AAG GAC ATG TTC AAT GTG AAC GTG CTG GCC CTC AGC ATC TGC ACA CGG GAA GCC TAC 399
Q S M K E R N V D D G H I I N I N S M S 153
CAG TCC ATG AAG GAG CGG AAT GTG GAC GAT GGG CAC ATC ATT AAC ATC AAT AGC ATG TCT 459
G H R V L P L S V T H F Y S A T K Y A V 173
GGC CAC CGA GTG TTA CCC CTG TCT GTG ACC CAC TTC TAT AGT GCC ACC AAG TAT GCC GTC 519
T A L T E G L R Q E L R E A Q T H I R A 193
ACT GCG CTG ACA GAG GGA CTG AGG CAA GAG CTT CGG GAG GCC CAG ACC CAC ATC CGA GCC 579
T C I S P G V V E T Q F A F K L H D K D 213
ACG TGC ATC TCT CCA GGT GTG GTG GAG ACA CAA TTC GCC TTC AAA CTC CAC GAC AAG GAC 639
P E K A A A T Y E Q M K C L K P E D V A 233
CCT GAG AAG GCA GCT GCC ACC TAT GAG CAA ATG AAG TGT CTC AAA CCC GAG GAT GTG GCC 699
E A V I Y V L S T P A H I Q I G D I Q M 253
GAG GCT GTT ATC TAC GTC CTC AGC ACT CCC GCA CAC ATC CAG ATT GGA GAC ATC CAG ATG 759
R P T E Q V T *
AGG CCC ACG GAG CAG GTG ACC TAG 261
873
TGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCCTTCATGGCTTGCCCTCCTGCCCTCTGGATTTTAGGTGTTGATTTCTGG
ATCACGGGATACCACTTCCTGTCCACACCCCGACCAGGGGCTAGAAAAATTTGTTTGAGATTTTATATCATCTTGTCAA
ATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCCTAATTGTTTACTTGTAACTTGTTC

```

FIGURE 1

TTGTGCCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCC  
CCATCTTCTTGCACCTCAACGTCTGTGGCTYANGGGCTGGGGTGGCAGAGGGAGGCCTTCACCTTATATCTGTGTGT  
ATCCAGGGCTCCAGACTTCCCTCTCTGCTGCCCCACTGCACCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAG  
CCCAGTCTTGGCTTCTTGTCCCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCT  
GGCCCAGTGGATTTCATGGTGATCATTAAGAAAGAAAAATCGCAACCAAAAAAAAAAAAAAAAAAGGGCGGGCCGCTAGAC  
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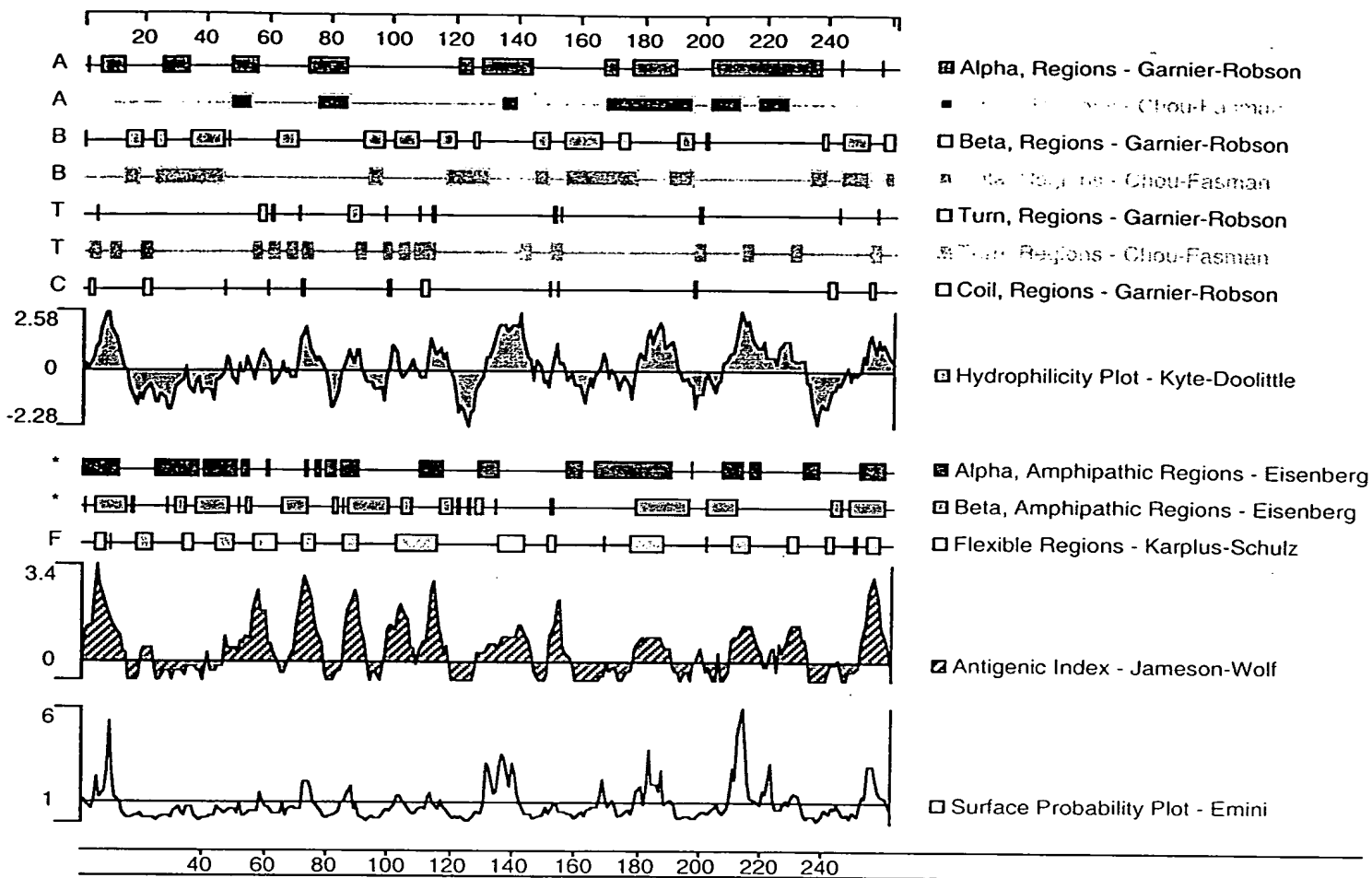
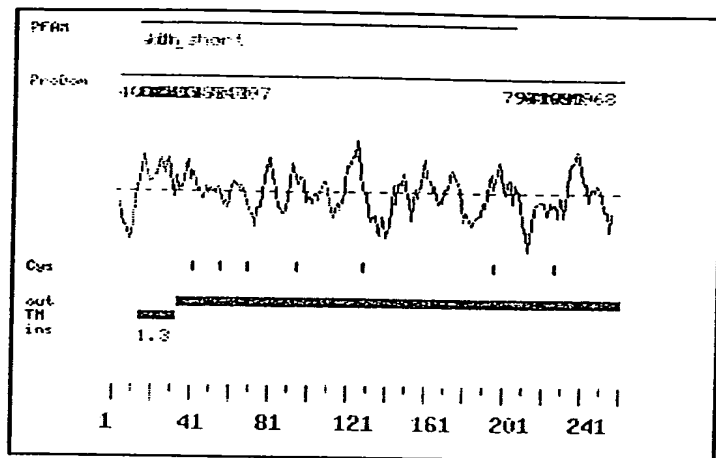


FIGURE 2

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## Analysis of 21620 (260 aa)



### Signal Peptide Predictions for 21620

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

### Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
13	32	ins-->out	1.3

FIGURE 3

## Prosite Pattern Matches 21620

>P300005|PDOC00005|PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 135      SMK      137

>P300006|PDOC00006|CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 72      SNEE      75

Query: 89      SGVD      92

Analysis of 21620

Query: 135      SMKE      138

>P300008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 18      GASGGI      23

Query: 24      GAAVAR      29

Query: 40      GCARTV      45

Query: 90      GVDICI      95

Query: 109      GSTSGW      114

Query: 199      GVVETQ      204

>P300061|PDOC00060|ADH\_SHORT Short-chain alcohol dehydrogenase family signature.

Query: 166      YSATKYAVTAL      176

FIGURE 4

ADH21620

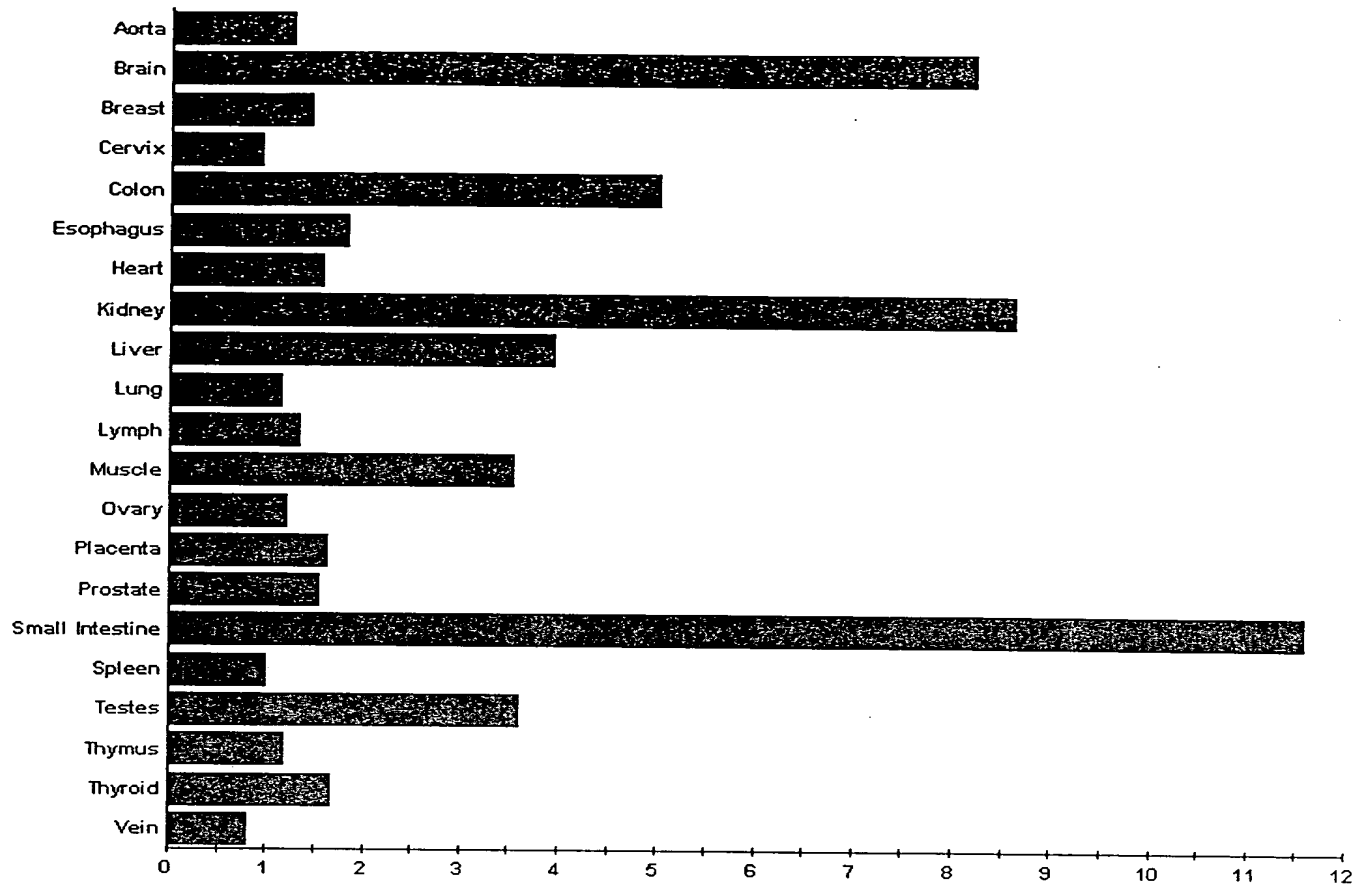


FIGURE 5

21620 Taqman Oncology Panel Expression

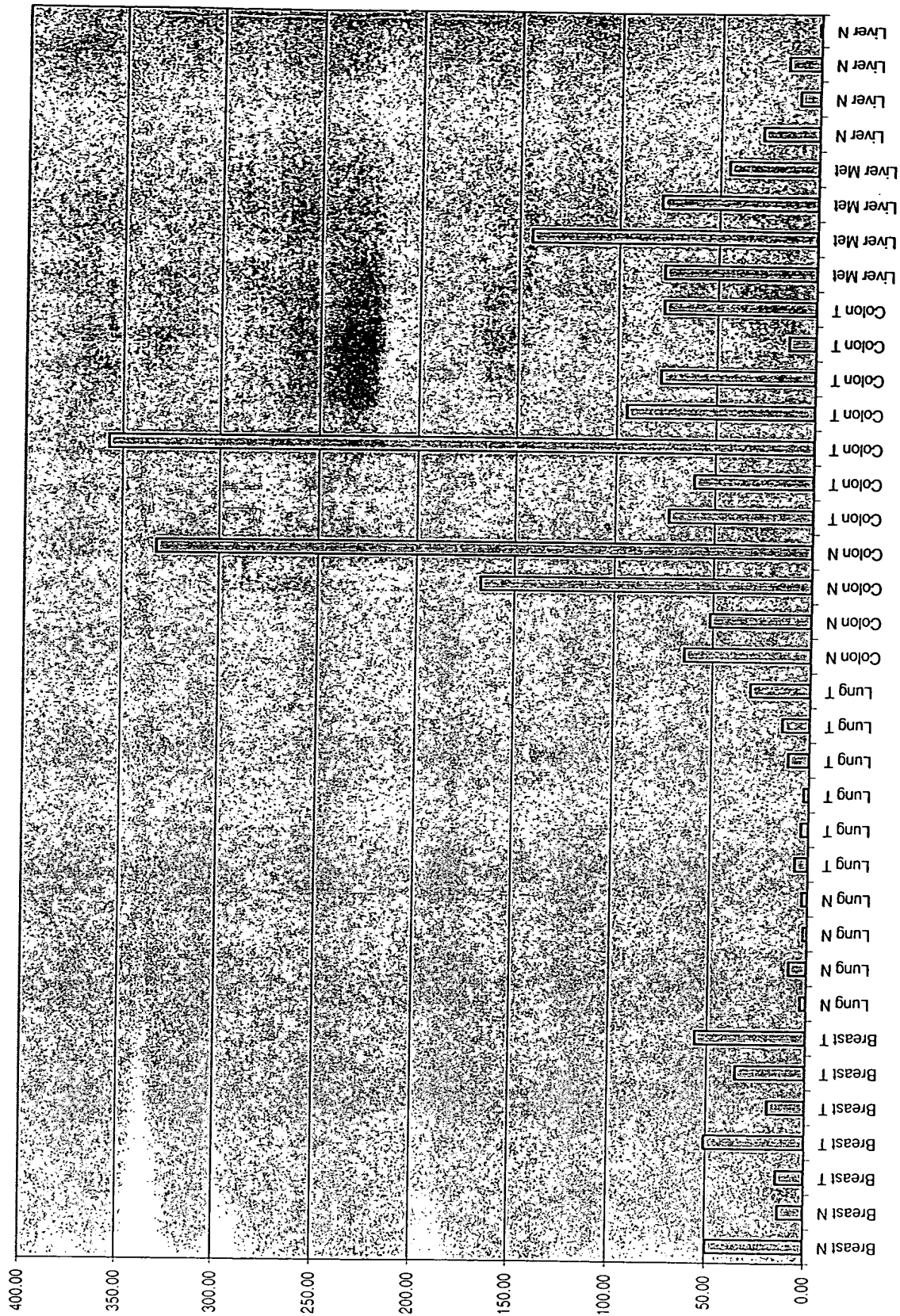


FIGURE 6

Input file Fbh33756.seq; Output File 33756.trans  
Sequence length 1153

CCGCGCCCCCGCCTCGCAGCCCANNTNCGGACGCGGGCCCAGCCGCGCCTGCGCTTCCGCTCGCCTGTGGCTGCAANNA

GCGCGCTCTTCTCGGAGCTACCCAGGCGGCTGGTGTAGCAGCAAGCTCCGCGCCGACCCCTGACGCCCTGACGCCCTGTC

CCCGGCCCCGCGCATGAGCGCTACCTGCTGCCGCTGTCCGCGCTGGGCACGGTAGCAGGCGCTGCCCGTGTGCTCAAGA

                  M  E  K  C  E  A  A  A  K  D  I  R  G      13  
GGCAACATCATCCTGGCCTGCCGAGAC  ATG  GAG  AAG  TGT  GAG  GCG  GCA  GCA  AAG  GAC  ATC  CGC  GGG      39

  E  T  L  N  H  H  V  N  A  R  H  L  D  L  A  S  L  K  S  I      33  
GAG  ACC  CTC  AAT  CAC  CAT  GTC  AAC  GCC  CGG  CAC  CTG  GAC  TTG  GCT  TCC  CTC  AAG  TCT  ATC      99

  R  E  F  A  A  K  I  I  E  E  E  E  R  V  D  I  L  I  N  N      53  
CGA  GAG  TTT  GCA  GCA  AAG  ATC  ATT  GAA  GAG  GAG  GAG  CGA  GTG  GAC  ATT  CTA  ATC  AAC  AAC     159

  A  G  V  M  R  C  P  H  W  T  T  E  D  G  F  E  M  Q  F  G      73  
GCG  GGT  GTG  ATG  CGG  TGC  CCC  CAC  TGG  ACC  ACC  GAG  GAC  GGC  TTC  GAG  ATG  CAG  TTT  GGC     219

  V  N  H  L  G  H  F  L  L  T  N  L  L  L  D  K  L  K  A  S      93  
GTT  AAC  CAC  CTG  GGT  CAC  TTT  CTC  TTG  ACA  AAC  TTG  CTG  CTG  GAC  AAG  CTG  AAA  GCC  TCA     279

  A  P  S  R  I  I  N  L  S  S  L  A  H  V  A  G  H  I  D  F     113  
GCC  CCT  TCG  CGG  ATC  ATC  AAC  CTC  TCG  TCC  CTG  GCC  CAT  GTT  GCT  GGG  CAC  ATA  GAC  TTT     339

  D  D  L  N  W  Q  T  R  K  Y  N  T  K  A  A  Y  C  Q  S  K     133  
GAC  GAC  TTG  AAC  TGG  CAG  ACG  AGG  AAG  TAT  AAC  ACC  AAA  GCC  GCC  TAC  TGC  CAG  AGC  AAG     399

  L  A  I  V  L  F  T  K  E  L  S  R  R  L  Q  G  S  G  V  T     153  
GTC  GCC  ATC  GTC  CTC  TTC  ACC  AAG  GAG  TTG  AGC  CGG  CGG  CTG  CAA  GGC  TCT  GGT  GTG  ACT     459

  V  N  A  L  H  P  G  V  A  R  T  E  L  G  R  H  T  G  I  H     173  
GTC  AAC  GCC  CTG  CAC  CCC  GGC  GTG  GCC  AGG  ACA  GAG  CTG  GGC  AGA  CAC  ACG  GGC  ATC  CAT     519

  G  S  T  F  S  S  T  T  L  G  P  I  F  W  L  L  V  K  S  P     193  
GGC  TCC  ACC  TTC  TCC  AGC  ACC  ACA  CTC  GGG  CCC  ATC  TTC  TGG  CTG  CTG  GTC  AAG  AGC  CCC     579

  E  L  A  A  Q  P  S  T  Y  L  A  V  A  E  E  L  A  D  V  S     213  
GAG  CTG  GCC  GCC  CAG  CCC  AGC  ACA  TAC  CTG  GCC  GTG  GCG  GAG  GAA  CTG  GCG  GAT  GTT  TCC     639

  G  K  Y  F  D  G  L  K  Q  K  A  P  A  P  E  A  E  D  E  E     233  
GGA  AAG  TAC  TTC  GAT  GGA  CTC  AAA  CAG  AAG  GCC  CCG  GCC  CCC  GAG  GCT  GAG  GAT  GAG  GAG     699

  V  A  R  R  L  W  A  E  S  A  R  L  V  G  L  E  A  P  S  V     253  
GTG  GCC  CGG  AGG  CTT  TGG  GCT  GAA  AGT  GCC  CGC  CTG  GTG  GGC  TTA  GAG  GCT  CCC  TCT  GTG     759

  R  E  Q  P  L  P  R  \*                                      261  
AGG  GAG  CAG  CCC  CTC  CCC  AGA  TAA                                     783

CCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAGACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCTGGCA

CTACCTGAGCCGGGAGACCCAGGACTG

FIGURE 7



100 200 300 400 500 600 700 800 900 1000 1100 1200 1300 1400 1500 1600 1700 1800 1900 2000 2100 2200 2300 2400 2500 2600 2700 2800 2900 3000 3100 3200 3300 3400 3500 3600 3700 3800 3900 4000 4100 4200 4300 4400 4500 4600 4700 4800 4900 5000 5100 5200 5300 5400 5500 5600 5700 5800 5900 6000 6100 6200 6300 6400 6500 6600 6700 6800 6900 7000 7100 7200 7300 7400 7500 7600 7700 7800 7900 8000 8100 8200 8300 8400 8500 8600 8700 8800 8900 9000 9100 9200 9300 9400 9500 9600 9700 9800 9900 10000

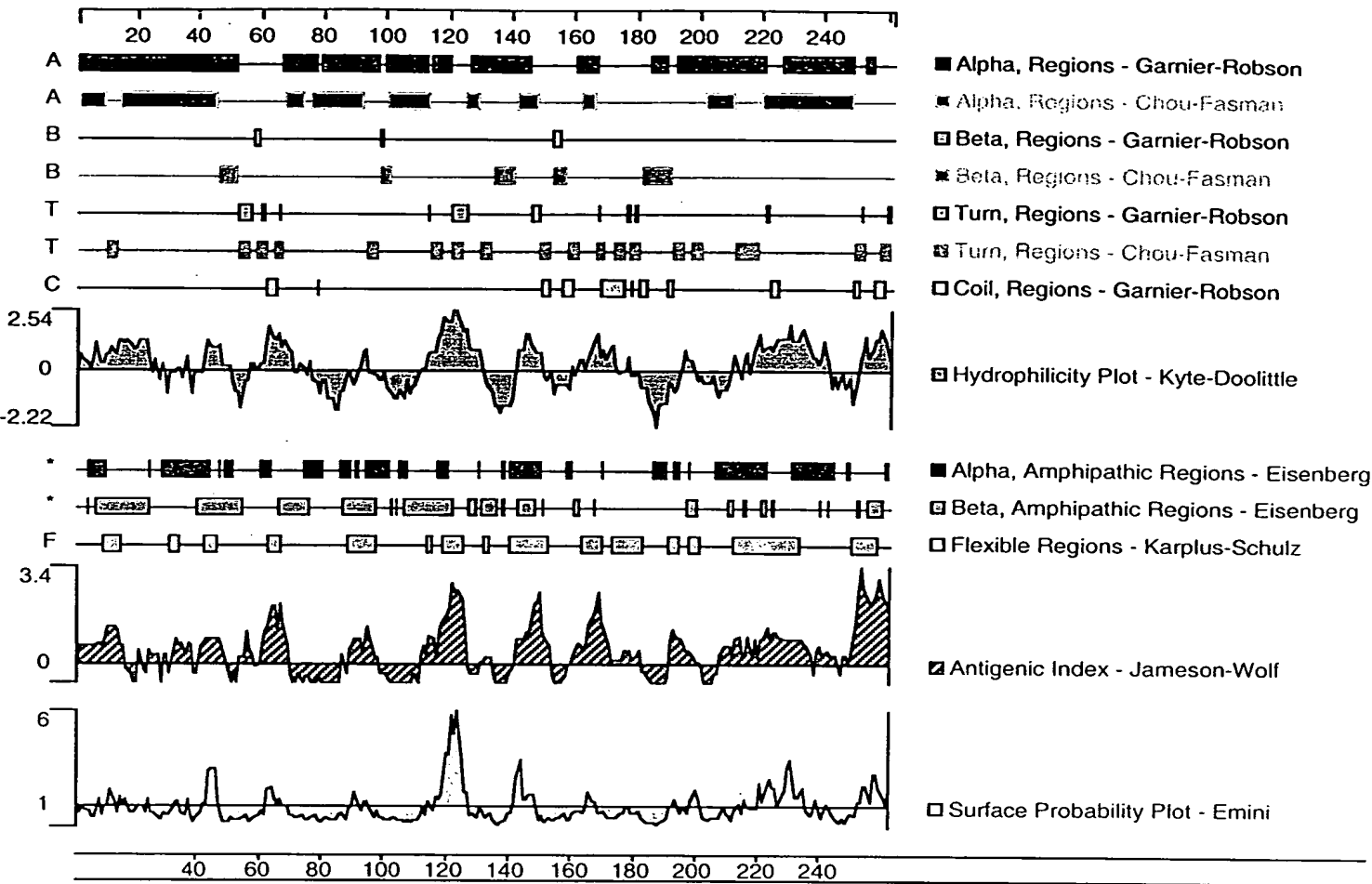
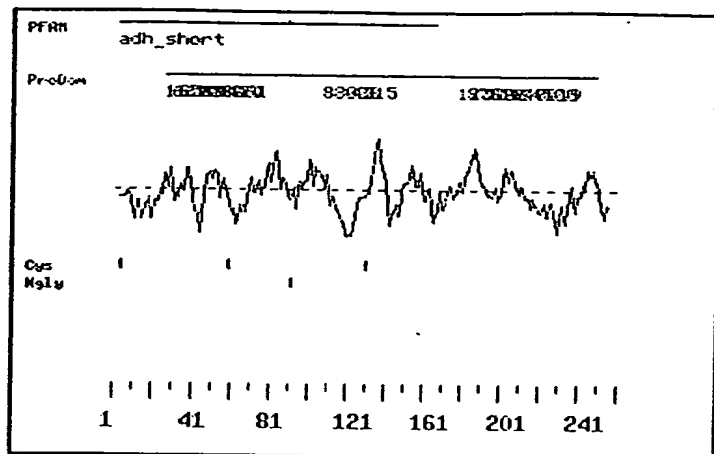


FIGURE 8

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## Analysis of 33756 (260 aa)



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### Signal Peptide Predictions for 33756

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

---

No TM domains predicted by MEMSAT for 33756

---

**FIGURE 9**

# Prosite Pattern Matches for 3

>PDOC00001|PDOC00001|ASN\_GLYCOSYLATION N-glycosylation site.

Query: 100 NLSS 103

>PDOC00005|PDOC00005|PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 29 SLK 31

Query: 32 SIR 34

Query: 120 TRK 122

Query: 144 SRR 146

Query: 213 SGK 215

Query: 242 SAR 244

Query: 252 SVR 254

>PDOC00006|PDOC00006|CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 32 SIRE 35

Query: 63 TTED 66

Query: 252 SVRE 255

>PDOC00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 149 GSGVTV 154

Query: 160 GVARTE 165

Query: 171 GIHGST 176

FIGURE 10

[illegible]

																	M	S	R	Y	4
GTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCGCTGACGCGCTGACGCGCTGTCCCCGGCCCCGGC																	ATG	AGC	CGC	TAC	12
L	L	P	L	S	A	L	G	T	V	A	G	A	A	V	L	L	K	D	Y	24	
CTG	CTG	CCG	CTG	TCG	GCG	CTG	GGC	ACG	GTA	GCA	GGC	GCC	GCC	GTG	CTG	CTC	AAG	GAC	TAT	72	
V	T	G	G	A	C	P	S	K	A	T	I	P	G	K	T	V	I	V	T	44	
GTC	ACC	GGT	GGG	GCT	TGC	CCC	AGC	AAG	GCC	ACC	ATC	CCT	GGG	AAG	ACG	GTC	ATC	GTG	ACG	132	
G	A	N	T	G	I	G	K	Q	T	A	L	E	L	A	R	R	G	G	N	64	
GGC	GCC	AAC	ACA	GGC	ATC	GGG	AAG	CAG	ACC	GCC	TTG	GAA	CTG	GCC	AGG	AGA	GGA	GGC	AAC	192	
I	I	L	A	C	R	D	M	E	K	C	E	A	A	A	K	D	I	R	G	84	
ATC	ATC	CTG	GCC	TGC	CGA	GAC	ATG	GAG	AAG	TGT	GAG	GCG	GCA	GCA	AAG	GAC	ATC	CGC	GGG	252	
E	T	L	N	H	H	V	N	A	R	H	L	D	L	A	S	L	K	S	I	104	
GAG	ACC	CTC	AAT	CAC	CAT	GTC	AAC	GCC	CGG	CAC	CTG	GAC	TTG	GCT	TCC	CTC	AAG	TCT	ATC	312	
R	E	F	A	A	K	I	I	E	E	E	E	R	V	D	I	L	I	N	N	124	
CGA	GAG	TTT	GCA	GCA	AAG	ATC	ATT	GAA	GAG	GAG	GAG	CGA	GTG	GAC	ATT	CTA	ATC	AAC	AAC	372	
A	G	V	M	R	C	P	H	W	T	T	E	D	G	F	E	M	Q	F	G	144	
GCG	GGT	GTG	ATG	CGG	TGC	CCC	CAC	TGG	ACC	ACC	GAG	GAC	GGC	TTC	GAG	ATG	CAG	TTT	GGC	432	
V	N	H	L	G	H	F	L	L	T	N	L	L	L	D	K	L	K	A	S	164	
GTT	AAC	CAC	CTG	GGT	CAC	TTT	CTC	TTG	ACA	AAC	TTG	CTG	CTG	GAC	AAG	CTG	AAA	GCC	TCA	492	
A	P	S	R	I	I	N	L	S	S	L	A	H	V	A	G	H	I	D	F	184	
GCC	CCT	TCG	CGG	ATC	ATC	AAC	CTC	TCG	TCC	CTG	GCC	CAT	GTT	GCT	GGG	CAC	ATA	GAC	TTT	552	
D	D	L	N	W	Q	T	R	K	Y	N	T	K	A	A	Y	C	Q	S	K	204	
GAC	GAC	TTG	AAC	TGG	CAG	ACG	AGG	AAG	TAT	AAC	ACC	AAA	GCC	GCC	TAC	TGC	CAG	AGC	AAG	612	
L	A	I	V	L	F	T	K	E	L	S	R	R	L	Q	G	S	G	V	T	224	
CTC	GCC	ATC	GTC	CTC	TTC	ACC	AAG	GAG	CTG	AGC	CGG	CGG	CTG	CAA	GGC	TCT	GGT	GTG	ACT	672	
V	N	A	L	H	P	G	V	A	R	T	E	L	G	R	H	T	G	I	H	244	
GTC	AAC	GCC	CTG	CAC	CCC	GGC	GTG	GCC	AGG	ACA	GAG	CTG	GGC	AGA	CAC	ACG	GGC	ATC	CAT	732	
G	S	T	F	S	S	T	T	L	G	P	I	F	W	L	L	V	K	S	P	264	
GGC	TCC	ACC	TTC	TCC	AGC	ACC	ACA	CTC	GGG	CCC	ATC	TTC	TGG	CTG	CTG	GTC	AAG	AGC	CCC	792	
E	L	V	A	Q	P	S	T	Y	L	A	V	A	E	E	L	A	D	V	S	284	
GAG	CTG	GTC	GCC	CAG	CCC	AGC	ACA	TAC	CTG	GCC	GTG	GCG	GAG	GAA	CTG	GCG	GAT	GTT	TCC	852	
G	K	Y	F	D	G	L	K	Q	K	A	P	A	P	E	A	E	D	E	E	304	

FIGURE 11

GGA AAG TAC TTC GAT GGA CTC AAA CAG AAG GCC CCG GCC CCC GAG GCT GAG GAT GAG GAG	912
V A R R L W A E S A R L V G L E A P S V	324
GTG GCC CGG AGG CTT TGG GCT GAA AGT GCC CGC CTG GTG GGC TTA GAG GCT CCC TCT GTG	972
R E Q P L P R *	332
AGG GAG CAG CCC CTC CCC AGA TAA	996

CCTCTGGAGCAGATTGAAAGCCAGGATGGCGCCTCCAGACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCTGGCA

CTACCTGAGCCGGGAGACCCAGGACTGGCGGCCGCTAGACTAGTCTAGAGAAAAACCTCCCACACCTCCCCCTGAACC

TGAAACAT

**FIGURE 11, Page 2**

21676.prot

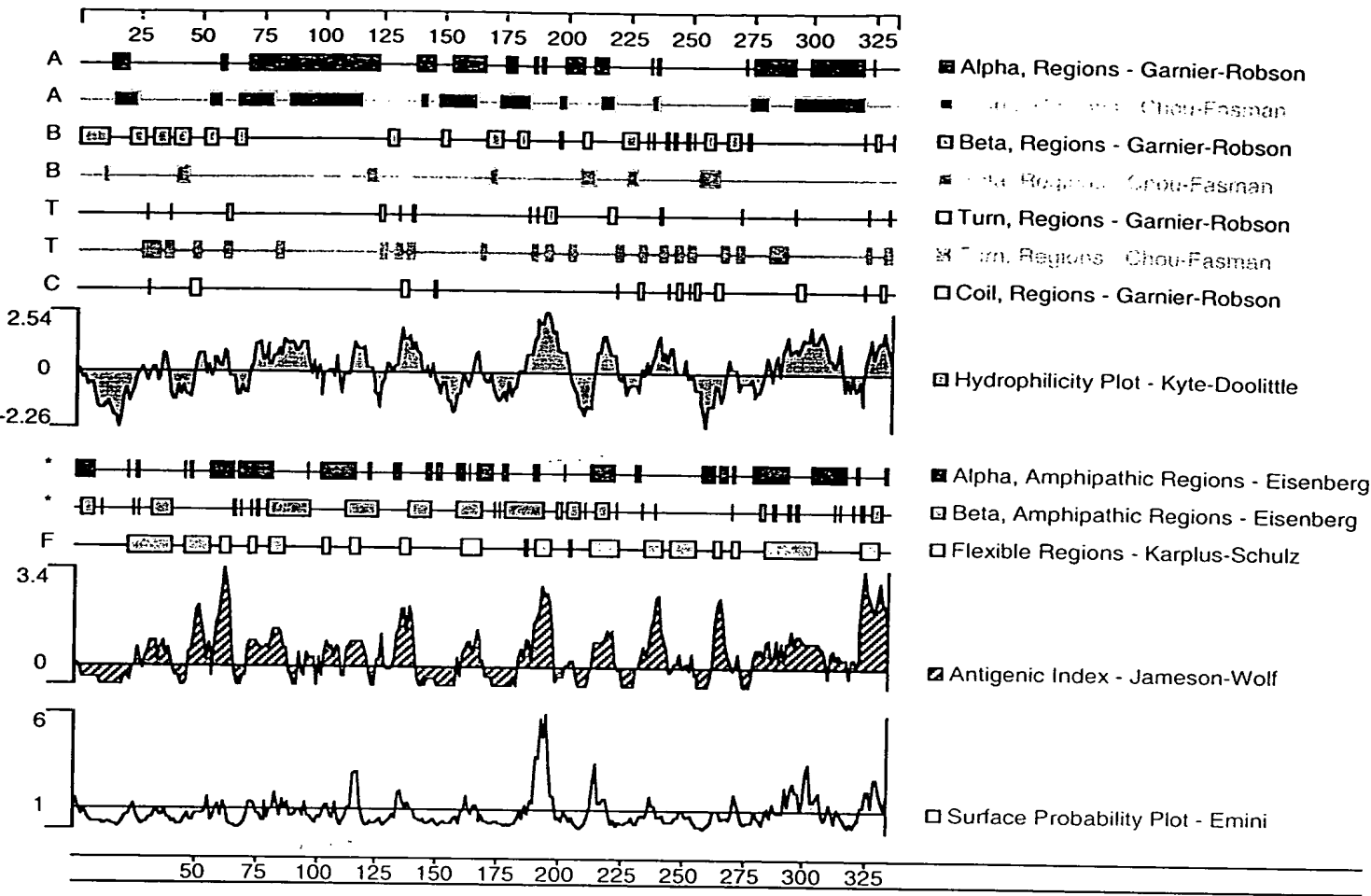
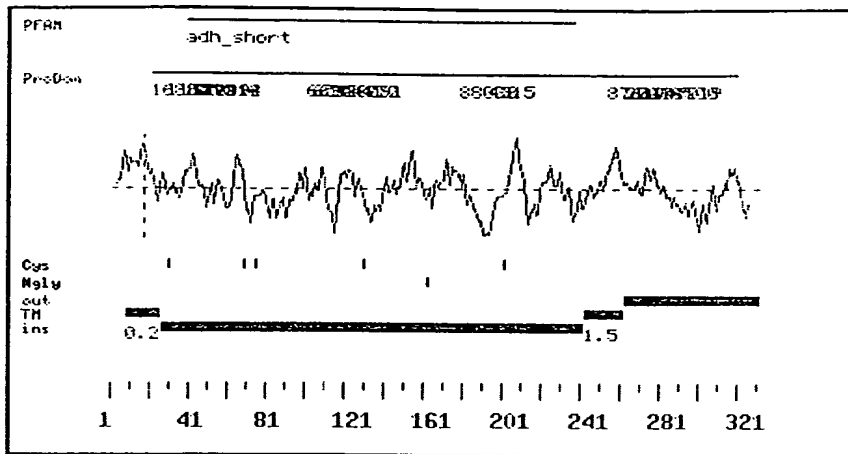


FIGURE 12

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## Analysis of 21676 (331 aa)



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### Signal Peptide Predictions for 21676

Method	Predict	Score	Mat@
SignalP (eukaryote)	YES		17

Note: amino-terminal 70aa used for signal peptide prediction

---

### Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
8	25	out-->ins	0.2
242	261	ins-->out	1.5

### Transmembrane segments for presumed mature peptide

Start	End	Orient	Score
226	245	out-->ins	2.1

## Prosites Pattern Matches for 21676

>PS00001|PDOC00001|ASN\_GLYCOSYLATION N-glycosylation site.

Query: 171      NLSS      174

>PS00005|PDOC00005|PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 100      SLK      102

Query: 103      SIR      105

Query: 191      TRK      193

Query: 215      SRR      217

Query: 284      SGK      286

Query: 313      SAR      315

Query: 323      SVR      325

>PS00006|PDOC00006|CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 54      TALE      57

Query: 103      SIRE      106

Query: 134      TTED      137

Query: 323      SVRE      326

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 12      GTVAGA      17

Query: 28      GACPSK      33

Query: 45      GANTGI      50

Query: 220      GSGVTV      225

Query: 231      GVARTE      236

Query: 242      GIHGST      247

FIGURE 14



Input file Fbh21612f11.seq; Output File 21612.trans  
Sequence length 2535

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AGGCAGAAGTATGCAAAGCATGCATCTCAAATTAGTCAGCAAACCATAGTCCCGGCCCTAACTCCGCCCATCCCGCCC
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TCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCTAGGCTTTTGCAAAAAGCTCCTCGATCGAG
GGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCTACCTGAGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCGGCC
TCCCGCCTGTGGTGCTCTCTGAAGTCGCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCG
GCGCTCCCTTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCCTTG
TTTCAGTTTTCTGTCTCTGCGCCGTTACAGATCCAAGCTCTGAAAAACCAGAAAGTTAACTGGTAAGTTTAGTCCTTTTG
TCTTTTATTTTCAGGTCCCGGATCCGGTGGTGGTGCAAAATCAAAGAACTGCTCCTCAGTGATGTTGCCCTTTACTTCTAG
GCCTGTACGGAAGTGTACTTCTGCTCTAAAAGCTGCGGAATTCTAATACGACTCACTATAGGGWGTGACCCACGCGT

                                M   L   P   N   T   G   R
CCGCTCGCCCGCCCGCTGTGCGCCGCCACCTCCTCTGATCTACGAAAGTC ATG TTA CCC AAC ACC GGG AGG      7
                                                                21

  L   A   G   C   T   V   F   I   T   G   A   S   R   G   I   G   K   A   I   A      27
CTG GCA GGA TGT ACA GTT TTT ATC ACA GGT GCA AGC CGT GGC ATT GGC AAA GCT ATT GCA      81

  L   K   A   A   K   D   G   A   N   I   V   I   A   A   K   T   A   Q   P   H      47
TTG AAA GCA GCA AAG GAT GGA GCA AAT ATT GTT ATT GCT GCA AAG ACC GCC CAG CCA CAT      141

  P   K   L   L   G   T   I   Y   T   A   A   E   E   I   E   A   V   G   G   K      67
CCA AAA CTT CTA GGC ACA ATC TAT ACT GCT GCT GAA GAA ATT GAA GCA GTT GGA GGA AAG      201

  A   L   P   C   I   V   D   V   R   D   E   Q   Q   I   S   A   A   V   E   K      87
GCC TTG CCA TGT ATT GTT GAT GTG AGA GAT GAA CAG CAG ATC AGT GCT GCA GTG GAG AAA      261

  A   I   K   K   F   G   G   I   D   I   L   V   N   N   A   S   A   I   S   L      107
GCC ATC AAG AAA TTT GGA GGA ATT GAT ATT CTG GTA AAT AAT GCC AGT GCC ATT AGT TTG      321

  T   N   T   L   D   T   P   T   K   R   L   D   L   M   M   N   V   N   T   R      127
ACC AAT ACA TTG GAC ACA CCT ACC AAG AGA TTG GAT CTG ATG ATG AAC GTG AAC ACC AGA      381

  G   T   Y   L   A   S   K   A   C   I   P   Y   L   K   K   S   K   V   A   H      147
GGC ACC TAC CTT GCA TCT AAA GCA TGT ATT CCT TAT TTG AAA AAG AGC AAA GTT GCT CAT      441

  I   L   N   I   S   P   P   L   N   L   N   P   V   W   F   K   Q   H   C   A      167
ATC CTC AAT ATC AGT CCA CCA CTG AAC CTA AAT CCA GTT TGG TTC AAA CAG CAC TGT GCT      501

  Y   T   I   A   K   Y   G   M   S   M   Y   V   L   G   M   A   E   E   F   K      187
TAT ACC ATT GCT AAG TAT GGT ATG TCT ATG TAT GTG CTT GGA ATG GCA GAA GAA TTT AAA      561

  G   E   I   A   V   N   A   L   W   P   K   T   A   I   H   T   A   A   M   D      207
GGT GAA ATT GCA GTC AAT GCA TTA TGG CCT AAA ACA GCC ATA CAC ACT GCT GCT ATG GAT      621

  M   L   G   G   P   G   I   E   S   Q   C   R   K   V   D   I   I   A   D   A      227
ATG CTG GGA GGA CCT GGT ATC GAA AGC CAG TGT AGA AAA GTT GAT ATC ATT GCA GAT GCA      681

  A   Y   S   I   F   Q   K   P   K   S   F   T   G   N   F   V   I   D   E   N      247
GCA TAT TCC ATT TTC CAA AAG CCA AAA AGT TTT ACT GGC AAC TTT GTC ATT GAT GAA AAT      741

  I   L   K   E   E   G   I   E   N   F   D   V   Y   A   I   K   P   G   H   P      267

```

FIGURE 15

ATC TTA AAA GAA GAA GGA ATA GAA AAT TTT GAC GTT TAT GCA ATT AAA CCA GGT CAT CCT	801
L Q P D F F L D E Y P E A V S K K V E S	287
TTG CAA CCA GAT TTC TTC TTA GAT GAA TAC CCA GAA GCA GTT AGC AAG AAA GTG GAA TCA	861
T G A V P E F K E E K L Q L Q P K P R S	307
ACT GGT GCT GTT CCA GAA TTC AAA GAA GAG AAA CTG CAG CTG CAA CCA AAA CCA CGT TCT	921
G A V E E T F R I V K D S L S D D V V K	327
GGA GCT GTG GAA GAA ACA TTT AGA ATT GTT AAG GAC TCT CTC AGT GAT GAT GTT GTT AAA	981
A T Q A I Y L F E L S G E D G G T W F L	347
GCC ACT CAA GCA ATC TAT CTG TTT GAA CTC TCC GGT GAA GAT GGT GGC ACG TGG TTT CTT	1041
D L K S K G G N V G Y G E P S D Q A D V	367
GAT CTG AAA AGC AAG GGT GGG AAT GTC GGA TAT GGA GAG CCT TCT GAT CAG GCA GAT GTG	1101
V M S M T T D D F V K M F S G K L K P T	387
GTG ATG AGT ATG ACT ACT GAT GAC TTT GTA AAA ATG TTT TCA GGG AAA CTA AAA CCA ACA	1161
M A F M S G K L K I K G N M A L A I K L	407
ATG GCA TTC ATG TCA GGG AAA TTG AAG ATT AAA GGT AAC ATG GCC CTA GCA ATC AAA TTG	1221
E K L M N Q M N A R L *	419
GAG AAG CTA ATG AAT CAG ATG AAT GCC AGA CTG TGA	1257

AGGAAAATATAAAAAAAGTCGACTGCTATGCTCAAAAAGTAAAAAAGCTCAACAGTTAAATCTAATGTTTGT  
 CTTTCTGTTATATTATAAGGATATGCACGTTTGTCTCGAAAAGATAGAATTGTCTCTAAAAGACTTGAAATGTAA  
 TTAAATGGCAAGCTAATCAAACATAAGCTTCATTAAGTGGGATCTAAGACAGTCGTGTTTTTATATTCAAGGGTT  
 TAACCCTTTGAGCCTTACATCTCATTCACTGTCTTTCTCCAAGAAAAGTATTTTGGGCGGACAGTCAGATCAAGCAGTA  
 AAATTAGCTCTTTCAAATCTTCTGTGTCATGTAATAAGCTAGTCTGTTTAAAATTTTAGTTTGGATTGTATACT  
 AATGAAAATCTTAATGATGTTTTRWTTTATATACYTAWTTTWAARRAAWYYTWWWWWRKWCMTTTTWMCAAAA  
 TWTTAAAAAWKRRWWWKRYTSKSGMGRASWMAWRWRAMMC

FIGURE 15, Page 2

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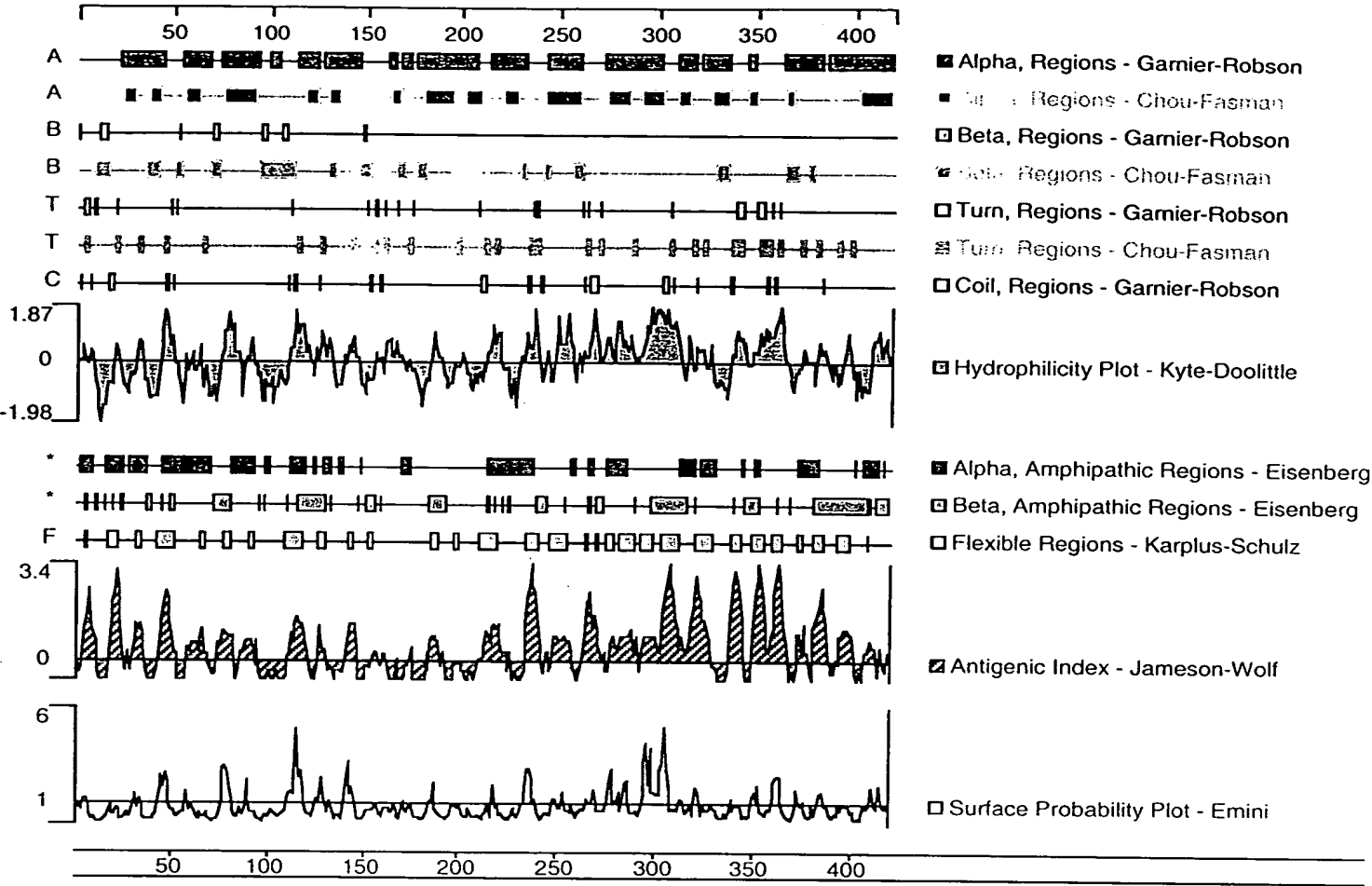
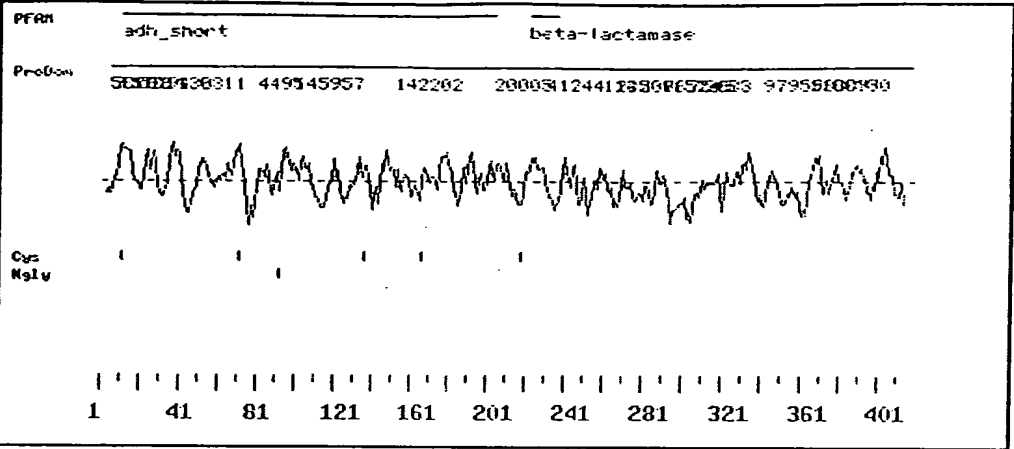


FIGURE 16

# Analysis of 21612 (418 aa)



## Signal Peptide Predictions for 21612

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

No TM domains predicted by MEMSAT for 21612

FIGURE 17

## Prosite Pattern Match for 21612

>PS00001|PDOC00001|ASN\_GLYCOSYLATION N-glycosylation site.

Query: 101 NASA 104

>PS00005|PDOC00005|PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 5 TGR 7

Query: 115 TKR 117

Query: 282 SKK 284

Query: 313 TFR 315

Query: 381 SGK 383

Query: 392 SGK 394

>PS00006|PDOC00006|CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 56 TAAE 59

Query: 320 SLSD 323

Query: 338 SGED 341

Query: 372 TTDD 375

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 17 GASRGI 22

Query: 52 GTIYTA 57

Query: 128 GTYLAS 133

Query: 353 GGNVGY 358

>PS00242|PDOC00299|MICROBODIES\_CTER Microbodies C-terminal targeting signal.

Query: 416 ARL 418

FIGURE 18

> Fbh21615a - Import - complete

```

1      ATGCAAAAGC CGAGNCCGCC TCGGCCTCTA AGCTATTCCA GAAGTAGTAA GAAGGCTTTT
61     TTGAAGGCCT AGGCTTTTGC AAAAAGCTCC TCGATCGAGG GGCTCGCATC TCTCCTTCAC
121    GGGGCCCGCG CCCTACCTGA GGCCGCCATC CACGCCGGTT GAGTCGCGTT CTGCCGCCTC
181    CCGCCTGTGG TGCCTCCTGA ACTGCGTCCG CCGTYTAGGT AAGTTTAAAG CTCAGGTCGA
241    GACCGGGCCT TTGTCCGGCG CTCCCTTGGA GCCTACCTAG ACTCAGCCGG CTCTCCACGC
301    TTTGCCTGAC CCTGCTTGCT CAACTCTACG TCTTTGTTTC GTTTTCTGTT CTGCGCCGTT
361    ACAGATCCAA GCTCTGAAAA ACCAGAAAGT TAACTGGTAA GTTTAGTCTT TTTGTCTTTT
421    ATTTCAGGTC CCGGATCCGG TGGTGGTGCA AATCAAAGAA CTGCTCCTCA GTGGATGTTG
481    CCTTTACTTC TAGGCCTGTA CGGAAGTGTT ACTTCTGCTC TAAAAGCTGC GGAATTCCTAA
541    TACGACTCAC TATAGGGAGT CGACCCACGC GTCCGCAAAC CGAGTTCTGG AGAACGCCAT
601    CAGCTCGCTG CTTAAAATTA AACCACAGGT TCCATTATGG GTCGACTTGA TGGGAAAGTC
661    ATCATCCTGA CGGCCGCTGC TCAGGGGATT GGCCAAGCAG CTGCCTTAGC TTTTGCAAGA
721    GAAGGTGCCA AAGTCATAGC CACAGACATT AATGAGTCCA AACTTCAGGA ACTGGAAAAG
781    TACCCGGGTA TTCAAACTCG TGTCCTTGAT GTCACAAAGA AGAAACAAAT TGATCAGTTT
841    GCCAATGAAG TTGAGAGACT TGATGTTCTC TTTAATGTTG CTGGTTTTGT CCATCATGGA
901    ACTGTCCTGG ATTGTGAGGA GAAAGACTGG GACTTCTCGA TGAATCTCAA TGTGCGCAGC
961    ATGTACCTGA TGATCAAGGC ATTCCTTCCT AAAATGCTTG CTCAGAAATC TGGCAATATT
1021   ATCAACATGT CTTCTGTGGC TTCCAGCGTC AAAGGAGTTG TGAACAGATG TGTGTACAGC
1081   ACAACCAAGG CAGCCGTGAT TGGCCTCACA AAATCTGTGG CTGCAGATTT CATCCAGCAG
1141   GGCATCAGGT GCAACTGTGT GTGCCCAGGA ACAGTTGATA CGCCATCTCT ACAAGAAAGA
1201   ATACAAGCCA GAGGAAATCC TGAAGAGGCA CGGAATGATT TCCTGAAGAG ACAAAGACG
1261   GGAAGATTTC CAACTGCAGA AGAAATAGCC ATGCTCTGCG TGTATTGGC TTCTGATGAA
1321   TCTGCTTATG TAACTGGTAA CCCTGTCATC ATTGATGGAG GCTGGAGCTT GTGATTTTAG
1381   GATCTCCATG GTGGGAAGGA AGGCAGGCC TTCCTATCCA CAGTGAACCT GGTACGAAG
1441   AAAACTCACC AATCATCTCC TTCCTGTTAA TCACATGTTA ATGAAAATAA GCTCTTTTAA
1501   ATGATGTCAC TGTTTGCAAG AGTCTGATTC TTTAAGTATA TTAATCTCTT TGTAATCTCT
1561   TCTGAAATCA TTGTAAAGAA ATAAAAATAT TGAACATAA AAAAAAAAAA AAAAAAGGGC
1621   GGCCGCTAGA CTAGTCTAGA GAAAAACCT CCCACACCTC CCCCTGAACC TGAAACATAA
1681   AATGAATGCM ATTGTTGKTG GTAACCTGTT ATTGCA

```

FIGURE 19A

> Fbh21615a - Import - complete

MGR~~ED~~DGKV IILTAAAQGI QAAAALAFAR  
EGAKVIATDI NESKLQELEK YPGIQTRVLD VTKKKQIDQF ANEVERLDVL FNVAGFVHHG  
TVLDCEEKDW DFSMNLNVRS MYLMIKAFLP KMLAQKSGNI INMSSVASSV KGVVNRVYS  
TTKAAVIGLT KSVAADFIQQ GIRCNCVCPG TVDTPSLQER IQARGNPEEA RNDFLKRQKT  
GRFATAEEIA MLCVYLASDE SAYVTGNPVI IDGGWSE\*

FIGURE 19B

21615prot

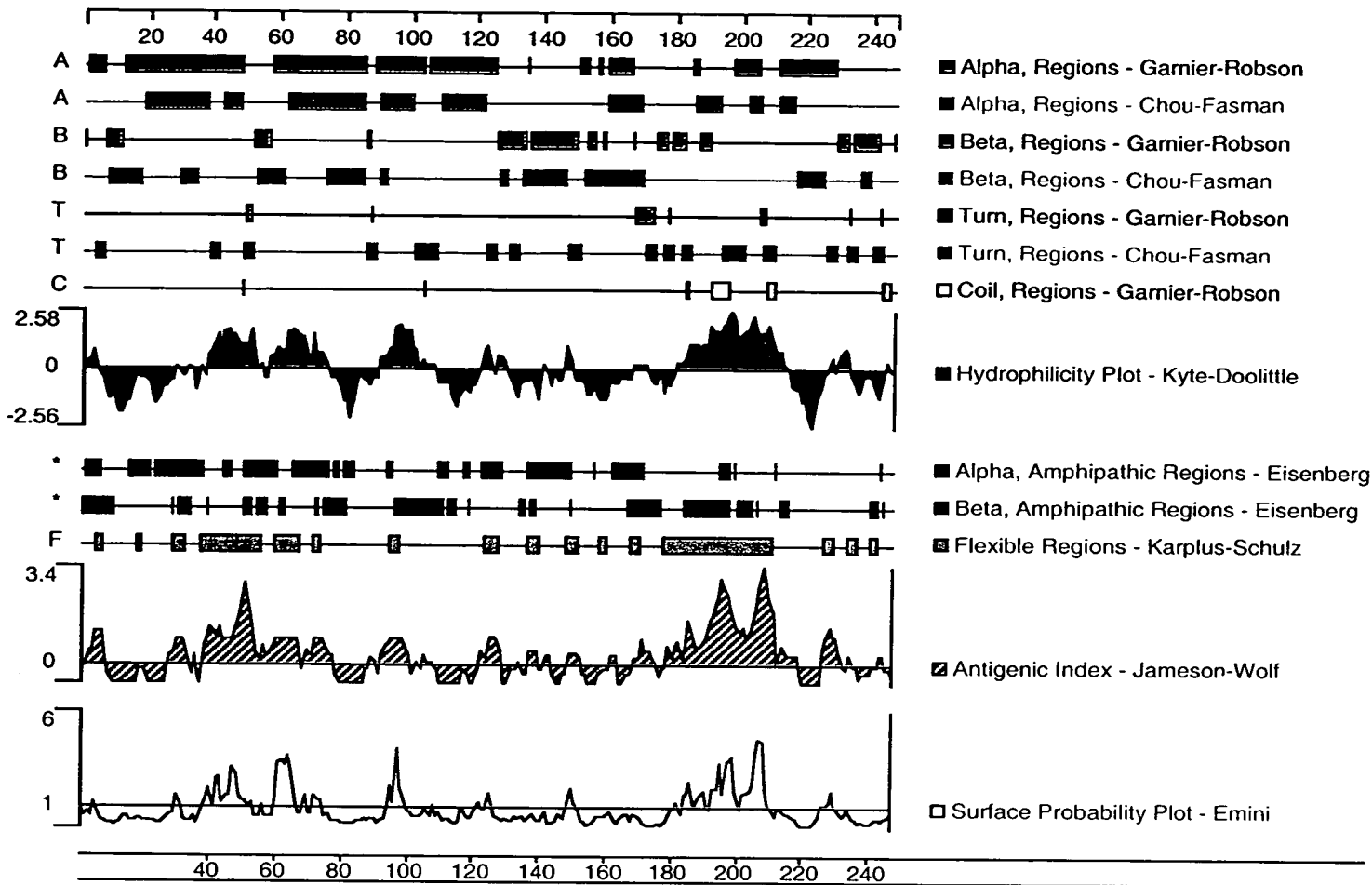
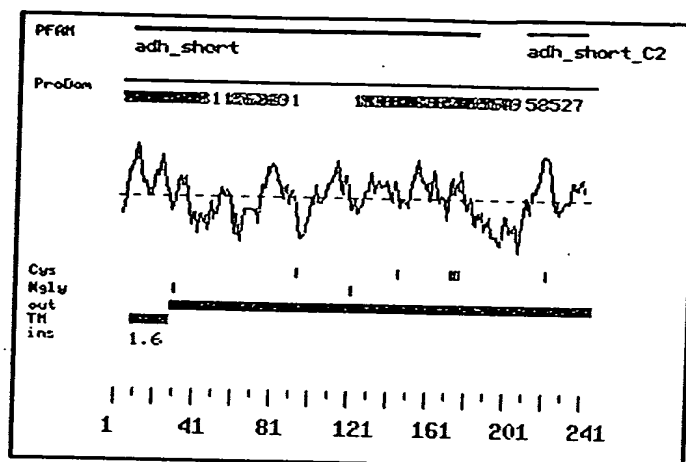


FIGURE 20



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## Analysis of 21615 (245 aa)



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### Signal Peptide Predictions for 21615

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

---

### Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
8	27	ins-->out	1.6

FIGURE 21

## Prosites Pattern Matches for 21615

>PS00001|PDOC00001|ASN\_GLYCOSYLATION N-glycosylation site.

Query: 39 NESK 42

Query: 130 NMSS 133

>PS00005|PDOC00005|PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 60 TTK 62

Query: 137 SVK 139

Query: 149 TTK 151

Query: 208 TGR 210

>PS00006|PDOC00006|CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 89 TVLD 92

Query: 184 SLQE 187

Query: 213 TAEE 216

>PS00007|PDOC00007|TYR\_PHOSPHO\_SITE Tyrosine kinase phosphorylation site.

Query: 42 KLQELEKY 49

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 17 GIGQAA 22

Query: 126 GNIINM 131

Query: 156 GLTKSV 161

Query: 169 GIRCNC 174

>PS00061|PDOC00060|ADH\_SHORT Short-chain alcohol dehydrogenase family signature.

Query: 147 YSTTKAAVIGL 157

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FIGURE 22

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